

Pur/09

Serial Number: 09/807,236

CRF Processing Date: 11/6/2001

Edited by:

Verified by: Ar

(STIC stat)

ENTERED

LB

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings-used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,236

DATE: 11/06/2001

TIME: 07:54:23

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\11062001\I807236.raw

P.S

3 <110> APPLICANT: E. I. du Pont de Nemours and Company
 5 <120> TITLE OF INVENTION: Plant Histidine Biosynthetic Enzymes
 7 <130> FILE REFERENCE: BB1255
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/807,236
 C--> 10 <141> CURRENT FILING DATE: 2001-07-23
 12 <150> PRIOR APPLICATION NUMBER: 60/105,409
 13 <151> PRIOR FILING DATE: 1998-10-23
 15 <160> NUMBER OF SEQ ID NOS: 22
 17 <170> SOFTWARE: Microsoft Office 97
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 433
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Zea mays
 24 <220> FEATURE:
 25 <221> NAME/KEY: unsure
 26 <222> LOCATION: (432)
 28 <400> SEQUENCE: 1
 29 gccgcctcct cccagccacc gcgctgccgc tgtccagcgc tcctcggcca gctccccagc 60
 30 gcgcagtcct agccgccgac cagcgccccc cgcgcagtc tagccgccgc gcagccgccg 120
 31 accagcgcct ctccggccag ctccctggcg tgcagtcct ccactagccg ccaagcacca 180
 32 ggaccacgcc atggccgtct gtctcccaaa gtatgtgttt agcgatggca agatgaacat 240
 33 tgaaaggctg acaaaacttg tcgagctggt tgggaaacag aggcttgtgc tggaccttaa 300
 34 gctgtcgaaa aaaggatggc aagatatact attgtaactg acaggtggca aaagttcagt 360
 35 gatgtgtttg tggatgaacc ggcattagaa tatctcgcgt cctttcgcag attagttttt 420
 36 tggttcatgg gng 433
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 74
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Zea mays
 43 <400> SEQUENCE: 2
 44 Gln Asp His Ala Met Ala Val Cys Leu Pro Lys Tyr Val Phe Ser Asp
 45 1 5 10 15
 47 Gly Lys Met Asn Ile Glu Arg Leu Thr Lys Leu Val Glu Leu Val Gly
 48 20 25 30
 50 Lys Gln Arg Leu Val Leu Asp Leu Lys Leu Ser Lys Lys Ala Arg Tyr
 51 35 40 45
 53 Thr Ile Val Thr Asp Arg Trp Gln Lys Phe Ser Asp Val Phe Val Asp
 54 50 55 60
 56 Glu Pro Ala Leu Glu Tyr Leu Ala Ala Phe
 57 65 70
 59 <210> SEQ ID NO: 3
 60 <211> LENGTH: 490
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Zea mays
 64 <220> FEATURE:
 65 <221> NAME/KEY: unsure
 66 <222> LOCATION: (261)

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Input Set : A:\PTO.AMC.txt

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68 <220> FEATURE:
69 <221> NAME/KEY: unsure
70 <222> LOCATION: (311)
72 <220> FEATURE:
73 <221> NAME/KEY: unsure
74 <222> LOCATION: (413)
76 <220> FEATURE:
77 <221> NAME/KEY: unsure
78 <222> LOCATION: (418)
80 <220> FEATURE:
81 <221> NAME/KEY: unsure
82 <222> LOCATION: (439)
84 <220> FEATURE:
85 <221> NAME/KEY: unsure
86 <222> LOCATION: (442)
88 <220> FEATURE:
89 <221> NAME/KEY: unsure
90 <222> LOCATION: (488)
92 <400> SEQUENCE: 3
93 gctagtatgt gaattgcagg ttaggaattg atgaggaact tgtggaacta ttggggcact 60
94 attcaccaat cccagtcact tatgctgggg gtgtgtcaac aatggacgac ctagagagga 120
95 taaagaaagc aggcaaaagt cgggtagatg taacaattgg gagtgctcta gatataattg 180
96 gaggagattt gccttacaaa gatgttgctc tttggcacag gaagcaaagt atggttggtc 240
W--> 97 aagtgtgaag aaacacaagg nattgatcag tattaccagt tcatttgatt caagcttctg 300
W--> 98 caciaagtat nttttctgaa catttttggt caaataattc aagttaggct atctccaaca 360
W--> 99 agatcctcct atctcctccc cctatttcaa acctattttg cgtcccctat ttntacanct 420
W--> 100 acactgggag acagtcctnc antgatgggt atctcaaate tgggggagca atgaccttgc 480
W--> 101 tttggggntt 490
103 <210> SEQ ID NO: 4
104 <211> LENGTH: 76
105 <212> TYPE: PRT
106 <213> ORGANISM: Zea mays
108 <400> SEQUENCE: 4
109 Arg Leu Gly Ile Asp Glu Glu Leu Val Glu Leu Leu Gly His Tyr Ser
110 1 5 10 15
112 Pro Ile Pro Val Thr Tyr Ala Gly Gly Val Ser Thr Met Asp Asp Leu
113 20 25 30
115 Glu Arg Ile Lys Lys Ala Gly Lys Ser Arg Val Asp Val Thr Ile Gly
116 35 40 45
118 Ser Ala Leu Asp Ile Phe Gly Gly Asp Leu Pro Tyr Lys Asp Val Val
119 50 55 60
121 Leu Trp His Arg Lys Gln Ser Met Val Gly Gln Val
122 65 70 75
124 <210> SEQ ID NO: 5
125 <211> LENGTH: 466
126 <212> TYPE: DNA
127 <213> ORGANISM: Zea mays
129 <400> SEQUENCE: 5
130 ggggttcgccg tcgcggcgcg gctacctcgc tccggctccc agctcgtccg gtccagctca 60

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131 ctgcggtcg cgaccatctc cgtccacctc atccctccgg caagcagttg ctaaactcat 120
132 ccagggtcag atcagcagct cttgccttat cccgctggct ggccgcagca ccggtggtgt 180
133 ggtggaggat ggcacgaaa tacgtggcca gggtagcgct tccatggtgg gcgccacaac 240
134 gtcgtttggt tggttcatgg gtttcgctct gctcggtaaa atgcggtgca ttgggaggac 300
135 ggatgttggt tgcgctgctg ttagcttcag accatgcacg gacattcaca aggggaaagt 360
136 taagcagatt gttggttcta ctcttcggga ttcattcaat gatggcatgg aacttgtagc 420
137 aaactttgaa tcagacaaat ctctgcaga atttgcaaaa tcatat 466

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139 <210> SEQ ID NO: 6

140 <211> LENGTH: 81

141 <212> TYPE: PRT

142 <213> ORGANISM: Zea mays

144 <400> SEQUENCE: 6

145 Met Val Gly Ala Thr Thr Ser Phe Gly Trp Phe Met Gly Phe Arg Leu

146 1 5 10 15

148 Leu Gly Lys Met Arg Cys Ile Gly Arg Thr Asp Val Val Cys Ala Ala

149 20 25 30

151 Val Ser Phe Arg Pro Cys Ile Asp Ile His Lys Gly Lys Val Lys Gln

152 35 40 45

154 Ile Val Gly Ser Thr Leu Arg Asp Ser Ser Asn Asp Gly Met Glu Leu

155 50 55 60

157 Val Thr Asn Phe Glu Ser Asp Lys Ser Pro Ala Glu Phe Ala Lys Ser

158 65 70 75 80

160 Tyr

163 <210> SEQ ID NO: 7

164 <211> LENGTH: 566

165 <212> TYPE: DNA

166 <213> ORGANISM: Zea mays

168 <220> FEATURE:

169 <221> NAME/KEY: unsure

170 <222> LOCATION: (326)

172 <220> FEATURE:

173 <221> NAME/KEY: unsure

174 <222> LOCATION: (340)

176 <220> FEATURE:

177 <221> NAME/KEY: unsure

178 <222> LOCATION: (383)

180 <220> FEATURE:

181 <221> NAME/KEY: unsure

182 <222> LOCATION: (398)

184 <220> FEATURE:

185 <221> NAME/KEY: unsure

186 <222> LOCATION: (418)

188 <220> FEATURE:

189 <221> NAME/KEY: unsure

190 <222> LOCATION: (437)

192 <220> FEATURE:

193 <221> NAME/KEY: unsure

194 <222> LOCATION: (443)..(444)

196 <220> FEATURE:

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197 <221> NAME/KEY: unsure
198 <222> LOCATION: (485)
200 <220> FEATURE:
201 <221> NAME/KEY: unsure
202 <222> LOCATION: (488)
204 <220> FEATURE:
205 <221> NAME/KEY: unsure
206 <222> LOCATION: (516)
208 <220> FEATURE:
209 <221> NAME/KEY: unsure
210 <222> LOCATION: (522)
212 <220> FEATURE:
213 <221> NAME/KEY: unsure
214 <222> LOCATION: (539)
216 <220> FEATURE:
217 <221> NAME/KEY: unsure
218 <222> LOCATION: (551)
220 <400> SEQUENCE: 7
221 cgtgctggac ctcagttgtc gaaaaaagga tggccgatat accattgtaa ctgacagggtg 60
222 gcaaaaagttc agtgatgtgt ttgtggatga accaacatta gaatatctcg ctgcctttgc 120
223 agatgagttt ttggttcattg gtgttgatgt ggagggcaaa aggttaggaa ttgatgagga 180
224 acttggtgaa ctattggggc actattcacc aatcccagtc acttatgctg ggggtgtgtc 240
225 aacaatggac gacctagaga ggataaagaa agcaggcaaa agtcgggtag atgtaacaat 300
W--> 226 tgggagtgtc ctatatataa ttggangaga ttgccttacn aagatgttgt ccttggcacc 360
W--> 227 agggagccaa gtaatgggtg gghcaagtgt gaagaachcc agggaattaa tccagtanta 420
W--> 228 cccagttcca ttgatnaaa ccnctggac caaaagataa ttccccgaa ccaatttttg 480
W--> 229 gtccnaanaa atccaggtaa ggggaatttc ccaanaaaag anccccctaa cccaaccnc 540
W--> 230 cccaatttcc naaaaccaa attttc 566
232 <210> SEQ ID NO: 8
233 <211> LENGTH: 108
234 <212> TYPE: PRT
235 <213> ORGANISM: Zea mays
237 <400> SEQUENCE: 8
238 Val Leu Asp Leu Ser Cys Arg Lys Lys Asp Gly Arg Tyr Thr Ile Val
239 1 5 10 15
241 Thr Asp Arg Trp Gln Lys Phe Ser Asp Val Phe Val Asp Glu Pro Thr
242 20 25 30
244 Leu Glu Tyr Leu Ala Ala Phe Ala Asp Glu Phe Leu Val His Gly Val
245 35 40 45
247 Asp Val Glu Gly Lys Arg Leu Gly Ile Asp Glu Glu Leu Val Glu Leu
248 50 55 60
250 Leu Gly His Tyr Ser Pro Ile Pro Val Thr Tyr Ala Gly Gly Val Ser
251 65 70 75 80
253 Thr Met Asp Asp Leu Glu Arg Ile Lys Lys Ala Gly Lys Ser Arg Val
254 85 90 95
256 Asp Val Thr Ile Gly Ser Ala Leu Asp Ile Ile Gly
257 100 105
259 <210> SEQ ID NO: 9
260 <211> LENGTH: 397

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261 <212> TYPE: DNA
262 <213> ORGANISM: Zea mays
264 <400> SEQUENCE: 9
265 cacaagggga aagttaagca gattgttggt tctactcttc gggattcatc caatgatggc 60
266 atggaacttg tgacaaactt tgaatcagac aaatctcctg cagaatttgc aaaatcatat 120
267 aaagaagatg aacttcttgg aggacatggt ataatgcttg gctcagatcc tgcaagccag 180
268 gctgctgcac tcgaggcact acatgcataat cctgggtggc tgcaagttgg aggtggaata 240
269 aatttgcaga atgcaatgtc ttaccttaat gaaggggcca gtcatgtgat agtgacctct 300
270 tatgtgttta gcgatggcaa gatgaacatt gaaaggctga caaaacttgt cgagctgggt 360
271 gggaaacaga gcttgtgctg gaccttagct gtcgaaa 397
273 <210> SEQ ID NO: 10
274 <211> LENGTH: 130
275 <212> TYPE: PRT
276 <213> ORGANISM: Zea mays
278 <400> SEQUENCE: 10
279 His Lys Gly Lys Val Lys Gln Ile Val Gly Ser Thr Leu Arg Asp Ser
280 1 5 10 15
282 Ser Asn Asp Gly Met Glu Leu Val Thr Asn Phe Glu Ser Asp Lys Ser
283 20 25 30
285 Pro Ala Glu Phe Ala Lys Ser Tyr Lys Glu Asp Glu Leu Leu Gly Gly
286 35 40 45
288 His Val Ile Met Leu Gly Ser Asp Pro Ala Ser Gln Ala Ala Ala Leu
289 50 55 60
291 Glu Ala Leu His Ala Tyr Pro Gly Gly Leu Gln Val Gly Gly Gly Ile
292 65 70 75 80
294 Asn Leu Gln Asn Ala Met Ser Tyr Leu Asn Glu Gly Ala Ser His Val
295 85 90 95
297 Ile Val Thr Ser Tyr Val Phe Ser Asp Gly Lys Met Asn Ile Glu Arg
298 100 105 110
300 Leu Thr Lys Leu Val Glu Leu Val Gly Lys Gln Ser Leu Cys Trp Thr
301 115 120 125
303 Leu Ala
304 130
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 423
308 <212> TYPE: DNA
309 <213> ORGANISM: Zea mays
311 <220> FEATURE:
312 <221> NAME/KEY: unsure
313 <222> LOCATION: (1)
315 <220> FEATURE:
316 <221> NAME/KEY: unsure
317 <222> LOCATION: (4)
319 <220> FEATURE:
320 <221> NAME/KEY: unsure
321 <222> LOCATION: (28)
323 <220> FEATURE:
324 <221> NAME/KEY: unsure
325 <222> LOCATION: (75)

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

WJ

VERIFICATION SUMMARY

DATE: 11/06/2001

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Input Set : A:\PTO.AMC.txt

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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:97 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:98 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:99 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:100 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:101 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:226 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:228 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:230 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:352 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:353 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:356 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:358 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:391 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:394 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:409 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:415 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:451 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:452 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:511 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

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L:514 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:585 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:586 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:612 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:615 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:624 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:682 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20